

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Weeks, Donald P.
Wang, Xiao-Zhuo
Herman, Patricia L.
- (ii) TITLE OF INVENTION: "METHODS AND MATERIALS FOR MAKING AND USING TRANSGENIC DICAMBA-DEGRADING ORGANISMS"
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sheridan Ross P.C.
 - (B) STREET: 1700 Lincoln St., Suite 3500
 - (C) CITY: Denver
 - (D) STATE: Colorado
 - (E) COUNTRY: USA
 - (F) ZIP: 80203
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/042,666
 - (B) FILING DATE: 04-APR-1997
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/042,941
 - (B) FILING DATE: 04-APR-1997
- (ix) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Crook, Wannell M.
 - (B) REGISTRATION NUMBER: 31,071
 - (C) REFERENCE/DOCKET NUMBER: 3553-18
- (x) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (303) 863-9700
 - (B) TELEFAX: (303) 863-0223

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 28
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Asp or Thr"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 29
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Pro"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Thr	Phe	Val	Arg	Asn	Ala	Trp	Tyr	Val	Ala	Ala	Leu	Pro	Glu	Glu	Leu
1						5			10						15
Ser	Glu	Lys	Pro	Leu	Gly	Arg	Thr	Ile	Leu	Asp	Xaa	Xaa			
				20					25						

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 8
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 16
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Thr	Tyr	Val	Val	Thr	Asp	Ala	Xaa	Ile	Lys	Xaa	Lys	Tyr	Met	Asp	Xaa
1				5					10				15		
Val Glu Val Xaa															
20															

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG	ACC	TTC	GTC	CGC	AAT	GCC	TGG	TAT	GTG	GCG	GCG	CTG	CCC	GAG	GAA	48
Met	Thr	Phe	Val	Arg	Asn	Ala	Trp	Tyr	Val	Ala	Leu	Pro	Glu	Glu		
1					5				10			15				
CTG TCC GAA AAG CCG CTC GGC CGG ACG ATT CTC GAC ACA CCG CTC GCG																
Leu	Ser	Glu	Lys	Pro	Leu	Gly	Arg	Thr	Ile	Leu	Asp	Thr	Pro	Leu	Ala	96
					20				25			30				
CTC TAC CGC CAG CCC GAC GGT GTG GTC GCG GCG CTG CTC GAC ATC TGT																
Leu	Tyr	Arg	Gln	Pro	Asp	Gly	Val	Val	Ala	Ala	Leu	Asp	Ile	Cys		144
					35			40			45					
CCG CAC CGC TTC GCG CCG CTG AGC GAC GGC ATC CTC GTC AAC GGC CAT																
Pro	His	Arg	Phe	Ala	Pro	Leu	Ser	Asp	Gly	Ile	Leu	Val	Asn	Gly	His	192
					50			55			60					
CTC CAA TGC CCC TAT CAC GGG CTG GAA TTC GAT GGC GGC GGG CAG TGC																
Leu	Gln	Cys	Pro	Tyr	His	Gly	Leu	Glu	Phe	Asp	Gly	Gly	Gln	Cys		240
					65			70			75			80		
GTC CAT AAC CCG CAC GGC AAT GGC GCC CGC CCG GCT TCG CTC AAC GTC																
Val	His	Asn	Pro	His	Gly	Asn	Gly	Ala	Arg	Pro	Ala	Ser	Leu	Asn	Val	288
					85			90			95					

CGC TCC TTC CCG GTG GTG GAG CGC GAC GCG CTG ATC TGG ATC TGG CCC Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro 100 105 110	336
GGC GAT CCG GCG CTG GCC GAT CCT GGG GCG ATC CCC GAC TTC GGC TGC Gly Asp Pro Ala Leu Ala Asp Pro Gly Ala Ile Pro Asp Phe Gly Cys 115 120 125	384
CGC GTC GAT CCC GCC TAT CGG ACC GTC GGC GGC TAT GGG CAT GTC GAC Arg Val Asp Pro Ala Tyr Arg Thr Val Gly Gly Tyr Gly His Val Asp 130 135 140	432
TGC AAC TAC AAG CTG CTG GTC GAC AAC CTG ATG GAC CTC GGC CAC GCC Cys Asn Tyr Lys Leu Leu Val Asp Asn Leu Met Asp Leu Gly His Ala 145 150 155 160	480
CAA TAT GTC CAT CGC AAC GCC CAG ACC GAC GCC TTC GAC CGG CTG Gln Tyr Val His Arg Ala Asn Ala Gln Thr Asp Ala Phe Asp Arg Leu 165 170 175	528
GAG CGC GAG GTG ATC GTC GGC GAC GGT GAG ATA CAG GCG CTG ATG AAG Glu Arg Glu Val Ile Val Gly Asp Gly Glu Ile Gln Ala Leu Met Lys 180 185 190	576
ATT CCC GGC GGC ACG CCG AGC GTG CTG ATG GCC AAG TTC CTG CGC GGC Ile Pro Gly Gly Thr Pro Ser Val Leu Met Ala Lys Phe Leu Arg Gly 195 200 205	624
GCC AAT ACC CCC GTC GCT TGG AAC GAC ATC CGC TGG AAC AAG GTG Ala Asn Thr Pro Val Asp Ala Trp Asn Asp Ile Arg Trp Asn Lys Val 210 215 220	672
AGC GCG ATG CTC AAC TTC ATC GCG GTG GCG CCG GAA GGC ACC CCG AAG Ser Ala Met Leu Asn Phe Ile Ala Val Ala Pro Glu Gly Thr Pro Lys 225 230 235 240	720
GAG CAG AGC ATC CAC TCG CGC GGT ACC CAT ATC CTG ACC CCC GAG ACG Glu Gln Ser Ile His Ser Arg Gly Thr His Ile Leu Thr Pro Glu Thr 245 250 255	768
GAG GCG AGC TGC CAT TAT TTC TTC GGC TCC TCG CGC AAT TTC GGC ATC Glu Ala Ser Cys His Tyr Phe Phe Gly Ser Ser Arg Asn Phe Gly Ile 260 265 270	816
GAC GAT CCG GAG ATG GAC GGC GTG CTG CGC AGC TGG CAG GCT CAG GCG Asp Asp Pro Glu Met Asp Gly Val Leu Arg Ser Trp Gln Ala Gln Ala 275 280 285	864
CTG GTC AAG GAG GAC AAG GTC GTC GAG GCG ATC GAG CGC CGC CGC Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg 290 295 300	912
GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TCG TGC GAC Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp 305 310 315 320	960

GAA GCC GCA GTC CGT GTC AGC CGC GAG ATC GAG AAG CTT GAG CAG CTC Glu Ala Ala Val Arg Val Ser Arg Glu Ile Glu Lys Leu Glu Gln Leu	1008
325 330 335	
GAA GCC GCC TGA Glu Ala Ala *	1020
340	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Thr	Phe	Val	Arg	Asn	Ala	Trp	Tyr	Val	Ala	Ala	Leu	Pro	Glu	Glu
1							5					10			15
Leu	Ser	Glu	Lys	Pro	Leu	Gly	Arg	Thr	Ile	Leu	Asp	Thr	Pro	Leu	Ala
									25					30	
Leu	Tyr	Arg	Gln	Pro	Asp	Gly	Val	Val	Ala	Ala	Leu	Leu	Asp	Ile	Cys
								35			40			45	
Pro	His	Arg	Phe	Ala	Pro	Leu	Ser	Asp	Gly	Ile	Leu	Val	Asn	Gly	His
								50			55			60	
Leu	Gln	Cys	Pro	Tyr	His	Gly	Leu	Glu	Phe	Asp	Gly	Gly	Gly	Gln	Cys
								65			70			75	
Val	His	Asn	Pro	His	Gly	Asn	Gly	Ala	Arg	Pro	Ala	Ser	Leu	Asn	Val
								85			90				95
Arg	Ser	Phe	Pro	Val	Val	Glu	Arg	Asp	Ala	Leu	Ile	Trp	Ile	Trp	Pro
								100			105			110	
Gly	Asp	Pro	Ala	Leu	Ala	Asp	Pro	Gly	Ala	Ile	Pro	Asp	Phe	Gly	Cys
								115			120			125	
Arg	Val	Asp	Pro	Ala	Tyr	Arg	Thr	Val	Gly	Gly	Tyr	Gly	His	Val	Asp
								130			135			140	
Cys	Asn	Tyr	Lys	Leu	Leu	Val	Asp	Asn	Leu	Met	Asp	Leu	Gly	His	Ala
									145			150			160
Gln	Tyr	Val	His	Arg	Ala	Asn	Ala	Gln	Thr	Asp	Ala	Phe	Asp	Arg	Leu
									165			170			175
Glu	Arg	Glu	Val	Ile	Val	Gly	Asp	Gly	Glu	Ile	Gln	Ala	Leu	Met	Lys
									180			185			190

Ile Pro Gly Gly Thr Pro Ser Val Leu Met Ala Lys Phe Leu Arg Gly
 195 200 205

Ala Asn Thr Pro Val Asp Ala Trp Asn Asp Ile Arg Trp Asn Lys Val
 210 215 220

Ser Ala Met Leu Asn Phe Ile Ala Val Ala Pro Glu Gly Thr Pro Lys
 225 230 235 240

Glu Gln Ser Ile His Ser Arg Gly Thr His Ile Leu Thr Pro Glu Thr
 245 250 255

Glu Ala Ser Cys His Tyr Phe Phe Gly Ser Ser Arg Asn Phe Gly Ile
 260 265 270

Asp Asp Pro Glu Met Asp Gly Val Leu Arg Ser Trp Gln Ala Gln Ala
 275 280 285

Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg
 290 295 300

Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
 305 310 315 320

Glu Ala Ala Val Arg Val Ser Arg Glu Ile Glu Lys Leu Glu Gln Leu
 325 330 335

Glu Ala Ala *
 340

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG ACC TAT GTC GTC ACC GAC GCC TGC ATC AAG TGC AAG TAC ATG GAC	48
Met Thr Tyr Val Val Thr Asp Ala Cys Ile Lys Cys Lys Tyr Met Asp	
1 5 10 15	
TGC GTG GAA GTC TGC CCT GTG GAC TGC TTC TAC GAA GGC GAG AAC ATG	96
Cys Val Glu Val Cys Pro Val Asp Cys Phe Tyr Glu Gly Glu Asn Met	
20 25 30	

CTC GTC ATC AAT CCC AGT GAA TGC ATC GAC TGC GGC GTC TGC GAA CCG Leu Val Ile Asn Pro Ser Glu Cys Ile Asp Cys Gly Val Cys Glu Pro 35 40 45	144
GAA TGC CCA GCC GAA GCC ATC CTT CCC GAC ACC GAA AGC GGT CTC GAG Glu Cys Pro Ala Glu Ala Ile Leu Pro Asp Thr Glu Ser Gly Leu Glu 50 55 60	192
CAG TGG ATG GAA CTG AAC ACG AAG TAC TCG GCC GAG TGG CCG AAT CTC Gln Trp Met Glu Leu Asn Thr Lys Tyr Ser Ala Glu Trp Pro Asn Leu 65 70 75 80	240
ACG TCC AAG AAA GAT TCG CCG GAA GAT GCC GAC GAG TAC AAG GGC GTG Thr Ser Lys Lys Asp Ser Pro Glu Asp Ala Asp Glu Tyr Lys Gly Val 85 90 95	288
GAA GGC AAG TTC GAG AAG TTC TTC TCG CCC GAG CCC GGC GAG GGC GAC Glu Gly Lys Phe Glu Lys Phe Phe Ser Pro Glu Pro Gly Glu Gly Asp 100 105 110	336
TGA *	339

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Tyr Val Val Thr Asp Ala Cys Ile Lys Cys Lys Tyr Met Asp 1 5 10 15
Cys Val Glu Val Cys Pro Val Asp Cys Phe Tyr Glu Gly Glu Asn Met 20 25 30
Leu Val Ile Asn Pro Ser Glu Cys Ile Asp Cys Gly Val Cys Glu Pro 35 40 45
Glu Cys Pro Ala Glu Ala Ile Leu Pro Asp Thr Glu Ser Gly Leu Glu 50 55 60
Gln Trp Met Glu Leu Asn Thr Lys Tyr Ser Ala Glu Trp Pro Asn Leu 65 70 75 80
Thr Ser Lys Lys Asp Ser Pro Glu Asp Ala Asp Glu Tyr Lys Gly Val 85 90 95
Glu Gly Lys Phe Glu Lys Phe Phe Ser Pro Glu Pro Gly Glu Gly Asp 100 105 110

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